WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254, over a region of at least about 100 residues, wherein the nucleic acid encodes at least one polypeptide having a protease activity, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

2. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63% or 64%.

3. The isolated or recombinant nucleic acid of claim 2, wherein the sequence identity is at least about 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or is 100%.

4. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, or the full length of a gene or a transcript.

5. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence comprises a sequence as set forth in SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254.

6. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence encodes a polypeptide having a sequence as set forth in SEQ ID NO:2; SEQ ID NO:4; SEQ ID NO:6; SEQ ID NO:8; SEQ ID NO:10; SEQ ID NO:12; SEQ ID NO:14; SEQ ID NO:16; SEQ ID NO:18; SEQ ID NO:20; SEQ ID NO:22; SEQ ID NO:24; SEQ ID NO:26; SEQ ID NO:28; SEQ ID NO:30; SEQ ID NO:32; SEQ ID NO:34; SEQ ID NO:36; SEQ ID NO:38; SEQ ID NO:40; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:52; SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID

NO:64; SEQ ID NO:66; SEQ ID NO:68; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID NO:78; SEQ ID NO:80; SEQ ID NO:82; SEQ ID NO:84; SEQ ID NO:86; SEQ ID NO:88; SEQ ID NO:90; SEQ ID NO:92; SEQ ID NO:94; SEQ ID NO:96; SEQ ID NO:98; SEQ ID NO:100; SEQ ID NO:102; SEQ ID NO:104; SEQ ID NO:106; SEQ ID NO:108; SEQ ID NO:110; SEQ ID NO:112; SEQ ID NO:114; SEQ ID NO:116; SEQ ID NO:118; SEQ ID NO:120; SEQ ID NO:122; SEQ ID NO:124; SEQ ID NO:126; SEQ ID NO:128; SEQ ID NO:130; SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; SEQ ID NO:147; SEQ ID NO:151; SEQ ID NO:159; SEQ ID NO:165; SEQ ID NO:172; SEQ ID NO:180; SEQ ID NO:188; SEQ ID NO:194; SEQ ID NO:200; SEQ ID NO:205; SEQ ID NO:211; SEQ ID NO:219; SEQ ID NO:223; SEQ ID NO:230; SEQ ID NO:235; SEQ ID NO:242; SEQ ID NO:249 or SEQ ID NO:255, or the polypeptide encoded by SEQ ID NO:145.

7. The isolated or recombinant nucleic acid of claim 1, wherein the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

8. The isolated or recombinant nucleic acid of claim 1, wherein the protease activity comprises catalyzing hydrolysis of peptide bonds.

9. The isolated or recombinant nucleic acid of claim 8, wherein the protease activity comprises an endoprotease activity or an exoprotease activity.

10. The isolated or recombinant nucleic acid of claim 8, wherein the protease activity comprises a proteinase activity or a peptidase activity.

11. The isolated or recombinant nucleic acid of claim 10, wherein the peptidase activity comprises a carboxypeptidase activity.

12. The isolated or recombinant nucleic acid of claim 10, wherein the peptidase activity comprises an aminopeptidase activity.

13. The isolated or recombinant nucleic acid of claim 1, wherein the protease activity comprises a serine protease activity.

14. The isolated or recombinant nucleic acid of claim 1, wherein the protease activity comprises a metalloprotease activity, a matrix metalloprotease activity or a collagenase activity.

15. The isolated or recombinant nucleic acid of claim 1, wherein the protease activity comprises a cysteine protease activity.

16. The isolated or recombinant nucleic acid of claim 1, wherein the protease activity comprises an aspartic protease activity.

17. The isolated or recombinant nucleic acid of claim 1, wherein the protease activity comprises a chymotrypsin, a trypsin, an elastase, a kallikrein or a subtilisin activity.

18. The isolated or recombinant nucleic acid of claim 1, wherein the protease activity comprises a peptidase activity.

19. The isolated or recombinant nucleic acid of claim 18, wherein the peptidase activity comprises a dipeptidylpeptidase activity.

20. The isolated or recombinant nucleic acid of claim 1, wherein the protease activity is thermostable.

21. The isolated or recombinant nucleic acid of claim 20, wherein the polypeptide retains a protease activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C.

22. The isolated or recombinant nucleic acid of claim 1, wherein the protease activity is thermotolerant.

23. The isolated or recombinant nucleic acid of claim 22, wherein the polypeptide retains a protease activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C.

24. An isolated or recombinant nucleic acid, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254, wherein the nucleic acid encodes a polypeptide having a protease activity.

25. The isolated or recombinant nucleic acid of claim 24, wherein the nucleic acid is at least about 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript.

26. The isolated or recombinant nucleic acid of claim 24, wherein the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

27. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide with a protease activity, wherein the probe comprises at least 10 consecutive bases of a sequence comprising SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254, wherein the probe identifies the nucleic acid by binding or hybridization.

28. The nucleic acid probe of claim 27, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

29. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a protease activity, wherein the probe comprises a nucleic acid comprising at least about 10 consecutive residues of SEQ ID NO:1; SEQ ID NO:3; SEQ

ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

30. The nucleic acid probe of claim 29, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

31. An amplification primer pair for amplifying a nucleic acid encoding a polypeptide having a protease activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

32. The amplification primer pair of claim 31, wherein a member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

33. An amplification primer pair, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the complementary strand of the first member.

34. A protease-encoding nucleic acid generated by amplification of a polynucleotide using an amplification primer pair as set forth in claim 33.

35. The protease-encoding nucleic acid of claim 34, wherein the amplification is by polymerase chain reaction (PCR).

36. The protease-encoding nucleic acid of claim 34, wherein the nucleic acid generated by amplification of a gene library.

37. The protease-encoding nucleic acid of claim 34, wherein the gene library is an environmental library.

38. An isolated or recombinant protease encoded by a protease-encoding nucleic acid as set forth in claim 34.

39. A method of amplifying a nucleic acid encoding a polypeptide having a protease activity comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

40. An expression cassette comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

41. A vector comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

42. A cloning vehicle comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

43. The cloning vehicle of claim 42, wherein the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector.

44. The cloning vehicle of claim 42, comprising a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

45. A transformed cell comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

46. A transformed cell comprising an expression cassette as set forth in claim 40.

47. The transformed cell of claim 40, wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

48. A transgenic non-human animal comprising a sequence as set forth in claim 1 or claim 24.

49. The transgenic non-human animal of claim 48, wherein the animal is a mouse.

50. A transgenic plant comprising a sequence as set forth in claim 1 or claim 24.

51. The transgenic plant of claim 50, wherein the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

52. A transgenic seed comprising a sequence as set forth in claim 1 or claim 24.

53. The transgenic seed of claim 52, wherein the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

54. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

55. The antisense oligonucleotide of claim 49, wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

56. A method of inhibiting the translation of a protease message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 24.

57. A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of a sequence as set forth in claim 1 or claim 24.

58. The double-stranded inhibitory RNA (RNAi) molecule of claim 52, wherein the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length.

59. A method of inhibiting the expression of a protease in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of a sequence as set forth in claim 1 or claim 24.

60. An isolated or recombinant polypeptide (i) having at least 50% sequence identity to SEQ ID NO:2; SEQ ID NO:4; SEQ ID NO:6; SEQ ID NO:8; SEQ ID NO:10; SEQ ID NO:12; SEQ ID NO:14; SEQ ID NO:16; SEQ ID NO:18; SEQ ID NO:20; SEQ ID NO:22; SEQ ID NO:24; SEQ ID NO:26; SEQ ID NO:28; SEQ ID NO:30; SEQ ID NO:32; SEQ ID NO:34; SEQ ID NO:36; SEQ ID NO:38; SEQ ID NO:40; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:52; SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; SEQ ID NO:66; SEQ ID NO:68; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID NO:78; SEQ ID NO:80; SEQ ID NO:82; SEQ ID NO:84; SEQ ID NO:86; SEQ ID NO:88; SEQ ID NO:90; SEQ ID NO:92; SEQ ID NO:94; SEQ ID NO:96; SEQ ID NO:98; SEQ ID NO:100; SEQ ID NO:102; SEQ ID NO:104; SEQ ID NO:106; SEQ ID NO:108; SEQ ID NO:110; SEQ ID NO:112; SEQ ID NO:114; SEQ ID NO:116; SEQ ID NO:118; SEQ ID NO:120; SEQ ID NO:122; SEQ ID NO:124; SEQ ID NO:126; SEQ ID NO:128; SEQ ID NO:130; SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; SEQ ID NO:147; SEQ ID NO:151; SEQ ID NO:159; SEQ ID NO:165; SEQ ID NO:172; SEQ ID NO:180; SEQ ID NO:188; SEQ ID

NO:194; SEQ ID NO:200; SEQ ID NO:205; SEQ ID NO:211; SEQ ID NO:219; SEQ ID NO:223; SEQ ID NO:230; SEQ ID NO:235; SEQ ID NO:242; SEQ ID NO:249 or SEQ ID NO:255, or the polypeptide encoded by SEQ ID NO:145, over a region of at least about 100 residues, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or, (ii) encoded by a nucleic acid having at least 50% sequence identity to a sequence as set forth in SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254, over a region of at least about 100 residues, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or encoded by a nucleic acid capable of hybridizing under stringent conditions to a sequence as set forth in SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID

NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254.

61. The isolated or recombinant polypeptide of claim 60, wherein the sequence identity is over a region of at least about at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or is 100% sequence identity.

62. The isolated or recombinant polypeptide of claim 60, wherein the sequence identity is over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050 or more residues, or the full length of an enzyme.

63. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide has a sequence as set forth in SEQ ID NO:2; SEQ ID NO:4; SEQ ID NO:6; SEQ ID NO:8; SEQ ID NO:10; SEQ ID NO:12; SEQ ID NO:14; SEQ ID NO:16; SEQ ID NO:18; SEQ ID NO:20; SEQ ID NO:22; SEQ ID NO:24; SEQ ID NO:26; SEQ ID NO:28; SEQ ID NO:30; SEQ ID NO:32; SEQ ID NO:34; SEQ ID NO:36; SEQ ID NO:38; SEQ ID NO:40; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:52; SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; SEQ ID NO:66; SEQ ID NO:68; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID

NO:78; SEQ ID NO:80; SEQ ID NO:82; SEQ ID NO:84; SEQ ID NO:86; SEQ ID NO:88; SEQ ID NO:90; SEQ ID NO:92; SEQ ID NO:94; SEQ ID NO:96; SEQ ID NO:98; SEQ ID NO:100; SEQ ID NO:102; SEQ ID NO:104; SEQ ID NO:106; SEQ ID NO:108; SEQ ID NO:110; SEQ ID NO:112; SEQ ID NO:114; SEQ ID NO:116; SEQ ID NO:118; SEQ ID NO:120; SEQ ID NO:122; SEQ ID NO:124; SEQ ID NO:126; SEQ ID NO:128; SEQ ID NO:130; SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; SEQ ID NO:147; SEQ ID NO:151; SEQ ID NO:159; SEQ ID NO:165; SEQ ID NO:172; SEQ ID NO:180; SEQ ID NO:188; SEQ ID NO:194; SEQ ID NO:200; SEQ ID NO:205; SEQ ID NO:211; SEQ ID NO:219; SEQ ID NO:223; SEQ ID NO:230; SEQ ID NO:235; SEQ ID NO:242; SEQ ID NO:249 or SEQ ID NO:255, or the polypeptide encoded by SEQ ID NO:145.

64. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide has a protease activity.

65. The isolated or recombinant polypeptide of claim 64, wherein the protease activity comprises catalyzing hydrolysis of peptide bonds.

66. The isolated or recombinant polypeptide of claim 65, wherein the protease activity comprises an endoprotease activity or an exoprotease activity.

67. The isolated or recombinant polypeptide of claim 65, wherein the protease activity comprises a proteinase activity or a peptidase activity.

68. The isolated or recombinant polypeptide of claim 67, wherein the peptidase activity comprises a carboxypeptidase activity.

69. The isolated or recombinant polypeptide of claim 67, wherein the peptidase activity comprises an aminopeptidase activity.

70. The isolated or recombinant polypeptide of claim 64, wherein the protease activity comprises a serine proteinase activity.

71. The isolated or recombinant polypeptide of claim 64, wherein the protease activity comprises a metalloproteinase activity, a matrix metalloproteinase activity or a collagenase activity.

72. The isolated or recombinant polypeptide of claim 64, wherein the protease activity comprises a cysteine protease activity.

73. The isolated or recombinant polypeptide of claim 64, wherein the protease activity comprises an aspartic protease activity.

74. The isolated or recombinant polypeptide of claim 64, wherein the protease activity comprises a chymotrypsin, a trypsin, an elastase, a kallikrein or a subtilisin activity.

75. The isolated or recombinant polypeptide of claim 64, wherein the protease activity comprises a peptidase activity.

76. The isolated or recombinant polypeptide of claim 64, wherein the peptidase activity comprises a dipeptidylpeptidase activity.

77. The isolated or recombinant polypeptide of claim 64, wherein the protease activity is thermostable.

78. The isolated or recombinant polypeptide of claim 77, wherein the polypeptide retains a protease activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 95°C, between about 70°C to about 75°C, or between about 90°C to about 95°C.

79. The isolated or recombinant polypeptide of claim 64, wherein the protease activity is thermotolerant.

80. The isolated or recombinant polypeptide of claim 79, wherein the polypeptide retains a protease activity after exposure to a temperature in the range from between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more.

81. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and lacking a signal sequence or a prepro sequence.

82. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and having a heterologous signal sequence or a heterologous prepro sequence.

83. The isolated or recombinant polypeptide of claim 64, wherein the protease activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein.

84. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of at least half of the specific activity of the protease at 37°C after being heated to an elevated temperature.

85. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature.

86. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises at least one glycosylation site.

87. The isolated or recombinant polypeptide of claim 86, wherein the glycosylation is an N-linked glycosylation.

88. The isolated or recombinant polypeptide of claim 87, wherein the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

89. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a protease activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0.

90. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a protease activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.

91. A protein preparation comprising a polypeptide as set forth in claim 60, wherein the protein preparation comprises a liquid, a solid or a gel.

92. A heterodimer comprising a polypeptide as set forth in claim 60 and a second domain.

93. The heterodimer of claim 92, wherein the second domain is a polypeptide and the heterodimer is a fusion protein.

94. The heterodimer of claim 92, wherein the second domain is an epitope or a tag.

95. A homodimer comprising a polypeptide as set forth in claim 60.

96. An immobilized polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 60, or a subsequence thereof.

97. The immobilized polypeptide of claim 96, wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

98. An array comprising an immobilized polypeptide as set forth in claim 60.

99. An array comprising an immobilized nucleic acid as set forth in claim 1 or claim 24.

100. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 60.

101. The isolated or recombinant antibody of claim 100, wherein the antibody is a monoclonal or a polyclonal antibody.

102. A hybridoma comprising an antibody that specifically binds to a polypeptide as set forth in claim 60.

103. A method of isolating or identifying a polypeptide with a protease activity comprising the steps of:

(a) providing an antibody as set forth in claim 100;

(b) providing a sample comprising polypeptides; and

(c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having a protease activity.

104. A method of making an anti-protease antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 or claim 24 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-protease antibody.

105. A method of making an anti-protease antibody comprising administering to a non-human animal a polypeptide as set forth in claim 60 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-protease antibody.

106. A method of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises a sequence as set forth in claim 1 or claim 24; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

107. The method of claim 106, further comprising transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

108. A method for identifying a polypeptide having a protease activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a protease substrate; and

(c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a protease activity.

109. A method for identifying a protease substrate comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a test substrate; and

(c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a protease substrate.

110. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has a sequence as set forth in claim 1 or claim 24;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

111. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) providing a polypeptide as set forth in claim 60;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

112. A method for identifying a modulator of a protease activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a test compound;

(c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the protease, wherein a change in the protease activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the protease activity.

113. The method of claim 112, wherein the protease activity is measured by providing a protease substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product.

114. The method of claim 113, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of protease activity.

115. The method of claim 113, wherein an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as

compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of protease activity.

116. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence as set forth in claim 60, a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

117. The computer system of claim 115, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

118. The computer system of claim 117, wherein the sequence comparison algorithm comprises a computer program that indicates polymorphisms.

119. The computer system of claim 117, further comprising an identifier that identifies one or more features in said sequence.

120. A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

121. A method for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) identifying one or more features in the sequence with the computer program.

122. A method for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide

sequence comprises a polypeptide as set forth in claim 60 or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) determining differences between the first sequence and the second sequence with the computer program.

123. The method of claim 122, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

124. The method of claim 123, further comprising an identifier that identifies one or more features in a sequence.

125. The method of claim 124, comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

126. A method for isolating or recovering a nucleic acid encoding a polypeptide with a protease activity from an environmental sample comprising the steps of:

(a) providing an amplification primer sequence pair as set forth in claim 31 or claim 33;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide with a protease activity from an environmental sample.

127. The method of claim 126, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence as set forth in SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID

NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254, or a subsequence thereof.

128. A method for isolating or recovering a nucleic acid encoding a polypeptide with a protease activity from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising a sequence as set forth in claim 1 or claim 24, or a subsequence thereof;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a protease activity from an environmental sample.

129. The method of claim 127 or claim 128, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample.

130. The method of claim 129, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

131. A method of generating a variant of a nucleic acid encoding a polypeptide with a protease activity comprising the steps of:

(a) providing a template nucleic acid comprising a sequence as set forth in claim 1 or claim 24; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid.

132. The method of claim 131, further comprising expressing the variant nucleic acid to generate a variant protease polypeptide.

133. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM), synthetic ligation reassembly (SLR) and a combination thereof.

134. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

135. The method of claim 131, wherein the method is iteratively repeated until a protease having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced.

136. The method of claim 135, wherein the variant protease polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature.

137. The method of claim 135, wherein the variant protease polypeptide has increased glycosylation as compared to the protease encoded by a template nucleic acid.

138. The method of claim 135, wherein the variant protease polypeptide has a protease activity under a high temperature, wherein the protease encoded by the template nucleic acid is not active under the high temperature.

139. The method of claim 131, wherein the method is iteratively repeated until a protease coding sequence having an altered codon usage from that of the template nucleic acid is produced.

140. The method of claim 131, wherein the method is iteratively repeated until a protease gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

141. A method for modifying codons in a nucleic acid encoding a polypeptide with a protease activity to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a protease activity comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

142. A method for modifying codons in a nucleic acid encoding a protease polypeptide, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a protease activity comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a protease.

143. A method for modifying codons in a nucleic acid encoding a protease polypeptide to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a protease polypeptide comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

144. A method for modifying a codon in a nucleic acid encoding a polypeptide having a protease activity to decrease its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a protease polypeptide comprising a sequence as set forth in claim 1 or claim 24; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell.

145. The method of claim 144, wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

146. A method for producing a library of nucleic acids encoding a plurality of modified protease active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a sequence as set forth in SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; SEQ ID NO:25; SEQ ID NO:27; SEQ ID NO:29; SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:35; SEQ ID NO:37; SEQ ID NO:39; SEQ ID NO:41; SEQ ID NO:43; SEQ ID NO:45; SEQ ID NO:47; SEQ ID NO:49; SEQ ID NO:51; SEQ ID NO:53; SEQ ID NO:55; SEQ ID NO:57; SEQ ID NO:59; SEQ ID NO:61; SEQ ID NO:63; SEQ ID NO:65; SEQ ID NO:67; SEQ ID NO:69; SEQ ID NO:71; SEQ ID NO:73; SEQ ID NO:75; SEQ ID NO:77; SEQ ID NO:79; SEQ ID NO:81; SEQ ID NO:83; SEQ ID NO:85; SEQ ID NO:87; SEQ ID NO:89; SEQ ID NO:91; SEQ ID NO:93; SEQ ID NO:95; SEQ ID NO:97; SEQ ID NO:99; SEQ ID NO:101; SEQ ID NO:103; SEQ ID NO:105; SEQ ID NO:107; SEQ ID NO:109; SEQ ID NO:111; SEQ ID NO:113; SEQ ID NO:115; SEQ ID NO:117; SEQ ID NO:119; SEQ ID NO:121; SEQ ID NO:123; SEQ ID NO:125; SEQ ID NO:127; SEQ ID NO:129; SEQ ID NO:131; SEQ ID NO:133; SEQ ID NO:135; SEQ ID NO:137; SEQ ID NO:139; SEQ ID NO:141; SEQ ID NO:143; SEQ ID NO:145; SEQ ID NO:146; SEQ ID NO:150; SEQ ID NO:158; SEQ ID NO:164; SEQ ID NO:171; SEQ ID NO:179; SEQ ID NO:187; SEQ ID NO:193; SEQ ID NO:199; SEQ ID NO:204; SEQ ID NO:210; SEQ ID NO:218; SEQ ID NO:222; SEQ ID NO:229; SEQ ID NO:234; SEQ ID NO:241; SEQ ID NO:248 or SEQ ID NO:254, or a subsequence thereof, and the nucleic acid encodes a protease active site or a protease substrate binding site;

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing

a library of nucleic acids encoding a plurality of modified protease active sites or substrate binding sites.

147. The method of claim 145, comprising mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, gene site-saturation mutagenesis (GSSM), or a synthetic ligation reassembly (SLR).

148. The method of claim 145, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM), synthetic ligation reassembly (SLR) and a combination thereof.

149. The method of claim 145, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

150. A method for making a small molecule comprising the following steps:

(a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises a protease enzyme encoded by a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;

(b) providing a substrate for at least one of the enzymes of step (a); and

(c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

151. A method for modifying a small molecule comprising the following steps:

(a) providing a protease enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence as set forth in claim 1 or claim 24;

(b) providing a small molecule; and

(c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the protease enzyme, thereby modifying a small molecule by a protease enzymatic reaction.

152. The method of claim 151, comprising a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the protease enzyme.

153. The method of claim 151, further comprising a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions.

154. The method of claim 153, further comprising the step of testing the library to determine if a particular modified small molecule which exhibits a desired activity is present within the library.

155. The method of claim 154, wherein the step of testing the library further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

156. A method for determining a functional fragment of a protease enzyme comprising the steps of:

(a) providing a protease enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and

(b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a protease activity, thereby determining a functional fragment of a protease enzyme.

157. The method of claim 156, wherein the protease activity is measured by providing a protease substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

158. A method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps:

(a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;

(b) culturing the modified cell to generate a plurality of modified cells;

(c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and,

(d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis.

159. The method of claim 158, wherein the genetic composition of the cell is modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene.

160. The method of claim 158, further comprising selecting a cell comprising a newly engineered phenotype.

161. The method of claim 160, further comprising culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

162. An isolated or recombinant signal sequence consisting of (i) a sequence as set forth in residues 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38 or 1 to 39 of SEQ ID NO:2; SEQ ID NO:4; SEQ ID NO:6; SEQ ID NO:8; SEQ ID NO:10; SEQ ID NO:12; SEQ ID NO:14; SEQ ID NO:16; SEQ ID NO:18; SEQ ID NO:20; SEQ ID NO:22; SEQ ID NO:24; SEQ ID NO:26; SEQ ID NO:28; SEQ ID NO:30; SEQ ID NO:32; SEQ ID NO:34; SEQ ID NO:36; SEQ ID NO:38; SEQ ID NO:40; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:52; SEQ ID NO:54; SEQ ID NO:56; SEQ ID NO:58; SEQ ID NO:60; SEQ ID NO:62; SEQ ID NO:64; SEQ ID NO:66; SEQ ID NO:68; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID NO:78; SEQ ID NO:80; SEQ ID NO:82; SEQ ID NO:84; SEQ ID NO:86; SEQ ID NO:88; SEQ ID NO:90; SEQ ID NO:92; SEQ ID NO:94; SEQ ID NO:96; SEQ ID NO:98; SEQ ID NO:100; SEQ ID NO:102; SEQ ID NO:104; SEQ ID NO:106; SEQ ID NO:108; SEQ ID NO:110; SEQ ID NO:112; SEQ ID NO:114; SEQ ID NO:116; SEQ ID NO:118; SEQ ID NO:120; SEQ ID NO:122; SEQ ID NO:124; SEQ ID NO:126; SEQ ID NO:128; SEQ ID NO:130; SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; SEQ ID NO:147; SEQ ID NO:151; SEQ ID NO:159; SEQ ID NO:165; SEQ ID NO:172; SEQ ID NO:180; SEQ ID NO:188; SEQ ID NO:194; SEQ ID NO:200; SEQ ID NO:205; SEQ ID NO:211; SEQ ID NO:219; SEQ ID NO:223; SEQ ID NO:230; SEQ ID NO:235; SEQ ID NO:242; SEQ ID NO:249 or SEQ ID NO:255, or the polypeptide encoded by SEQ ID NO:145, or, (ii) a signal sequence consisting of a sequence as set forth in Table 4.

163. A chimeric polypeptide comprising at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

164. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is not a protease.

165. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or a protease catalytic domain (CD).

166. An isolated or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162 and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

167. A method of increasing thermotolerance or thermostability of a protease polypeptide, the method comprising glycosylating a protease, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide as set forth in claim 60, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24, thereby increasing the thermotolerance or thermostability of the protease.

168. A method for overexpressing a recombinant protease in a cell comprising expressing a vector comprising a nucleic acid sequence as set forth in claim 1 or claim 24, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

169. A method of making a transgenic plant comprising the following steps:

(a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24, thereby producing a transformed plant cell;

(b) producing a transgenic plant from the transformed cell.

170. The method as set forth in claim 169, wherein the step (a) further comprises introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts.

171. The method as set forth in claim 169, wherein the step (a) comprises introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment or by using an *Agrobacterium tumefaciens* host.

172. A method of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps:

(a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24;

(b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

173. A method for hydrolyzing, breaking up or disrupting a protein-comprising composition comprising the following steps:

(a) providing a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a composition comprising a protein; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the protease hydrolyzes, breaks up or disrupts the protein-comprising composition.

174. The method as set forth in claim 173, wherein the composition comprises a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell.

175. A method for liquefying or removing a protein from a composition comprising the following steps:

(a) providing a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a composition comprising a protein; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the protease removes or liquefies the protein.

176. A detergent composition comprising a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24, wherein the polypeptide has a protease activity.

177. The detergent composition of claim 176, wherein the protease is a nonsurface-active protease or a surface-active protease.

178. The detergent composition of claim 176, wherein the protease is formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel form, a paste or a slurry form.

179. A method for washing an object comprising the following steps:

(a) providing a composition comprising a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing an object; and

(c) contacting the polypeptide of step (a) and the object of step (b) under conditions wherein the composition can wash the object.

180. A textile or fabric comprising a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

181. The method as set forth in claim 180, wherein the textile or fabric comprises a cellulose-containing fiber.

182. A method for removing protein stains from a composition comprising the following steps:

(a) providing a composition comprising a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a composition having a protein stain; and

(c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the protease can remove the stain.

183. A method for improving the finish of a fabric comprising the following steps:

(a) providing a composition comprising a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a fabric; and

(c) contacting the polypeptide of step (a) and the fabric of step (b) under conditions wherein the polypeptide can treat the fabric thereby improving the finish of the fabric.

184. The method as set forth in claim 183, wherein the fabric is a wool or a silk.

185. A feed or a food comprising a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

186. A method for hydrolyzing proteins in a feed or a food prior to consumption by an animal comprising the following steps:

(a) obtaining a feed material comprising a protease, wherein the protease has a sequence as set forth in claim 64, or is encoded by a nucleic acid as set forth in claim 1 or claim 24; and

(b) adding the polypeptide of step (a) to the feed or food material in an amount sufficient for a sufficient time period to cause hydrolysis of the protein and formation of a treated food or feed, thereby hydrolyzing the proteins in the food or the feed prior to consumption by the animal.

187. The method as set forth in claim 186, wherein the food or the feed is corn.

188. A method for improving texture and flavor of a dairy product comprising the following steps:

(a) providing a polypeptide having a protease activity, wherein the protease has a sequence as set forth in claim 64, or is encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a dairy product; and

(c) contacting the polypeptide of step (a) and the dairy product of step (b) under conditions wherein the protease can improve the texture or flavor of the dairy product.

189. The method as set forth in claim 188, wherein the dairy product comprises a cheese or a yogurt.

190. A dairy product comprising a protease having a sequence as set forth in claim 64, or is encoded by a nucleic acid as set forth in claim 1 or claim 24.

191. A method for tenderizing a meat or a fish comprising the following steps:

(a) providing a polypeptide having a protease activity, wherein the protease has a sequence as set forth in claim 64, or is encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a composition comprising meat or fish; and

(c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the polypeptide can tenderize the meat or the fish.

192. A method improving the extraction of oil from an oil-rich plant material comprising the following steps:

(a) providing a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing an oil-rich plant material; and

(c) contacting the polypeptide of step (a) with the oil-rich plant material under conditions wherein the polypeptide having a protease activity can catalyze the hydrolysis of a peptide bond.

193. The method of claim 220, wherein the oil-rich plant material comprises an oil-rich seed.

194. The method of claim 193, wherein the oil is a soybean oil, an olive oil, a rapeseed (canola) oil or a sunflower oil.

195. A method for preparing a fruit or vegetable juice, syrup, puree or extract comprising the following steps:

(a) providing a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a composition or a liquid comprising a fruit or vegetable material; and

(c) contacting the polypeptide of step (a) and the composition, thereby preparing the fruit or vegetable juice, syrup, puree or extract.

196. A paper or paper product or paper pulp comprising a protease as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

197. A method for treating a paper or a paper or wood pulp comprising the following steps:

(a) providing a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a composition comprising a paper or a paper or wood pulp; and

(c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the protease can treat the paper or paper or wood pulp.

198. A pharmaceutical composition comprising a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

199. The pharmaceutical composition of claim 198, wherein the pharmaceutical composition acts as a digestive aid or as a topical skin care.

200. A method of treating an imbalance of desquamation comprising topical application of the composition of claim 199.

201. The method of claim 199, wherein the treatment is prophylactic.

202. An oral care product comprising a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

203. The oral care product of claim 202, wherein the product comprises a toothpaste, a dental cream, a gel or a tooth powder, an odontic, a mouth wash, a pre- or post brushing rinse formulation, a chewing gum, a lozenge or a candy.

204. A contact lens cleaning composition comprising a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

205. A method for treating solid or liquid animal waste products comprising the following steps:

(a) providing a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a solid or a liquid animal waste; and

(c) contacting the polypeptide of step (a) and the solid or liquid waste of step (b) under conditions wherein the protease can treat the waste.

206. A processed waste product comprising a polypeptide having a protease activity, wherein the polypeptide comprises a sequence as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

207. A hairball remedy comprising a polypeptide having a protease activity, wherein the polypeptide comprises a sequence as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

208. A hairball prevention composition comprising a polypeptide having a protease activity, wherein the polypeptide comprises a sequence as set forth in claim 59, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

209. A blood or organic spot remover comprising a polypeptide having a protease activity, wherein the polypeptide comprises a sequence as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

210. A method for disinfecting a solid or a liquid comprising the following steps:

(a) providing a composition comprising a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a solid or a liquid to be disinfected; and

(c) contacting the composition of step (a) and the solid or liquid of step (b) under conditions wherein the protease can disinfect the solid or liquid.

211. The method of claim 210, wherein the composition of step (a) is formulated as a spray or a liquid.

212. An antimicrobial, anti-viral or anti-spore agent comprising a polypeptide having a protease activity, wherein the polypeptide comprises a sequence as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

213. A disinfectant comprising a polypeptide having a protease activity, wherein the polypeptide comprises a sequence as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

214. A method for tissue dissociation comprising the following steps:

(a) providing a composition comprising a polypeptide having a protease activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and

(b) contacting the composition of step (a) and with a tissue to be dissociated.

215. The method of claim 214, wherein the tissue of a wound.

216. The method of claim 214, wherein the contacting of step (b) is used for wound cleansing, wound bed preparation, to treat pressure ulcers, leg ulcers, burns, diabetic foot ulcers, scars, IV fixation, surgical wounds or minor wounds.

217. A medical dressing comprising a polypeptide having a protease activity, wherein the polypeptide comprises a sequence as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.